



**Fig. S1.** Linkage disequilibrium plot of 1504 biallelic sites across a ~399-kb genomic region at 1q42.2, based on datasets from JPT (Japanese in Tokyo) in the 1000 Genomes Project database. The position of SNPs examined is shown by the green arrow. The haplotype block was defined by the method of Gabriel *et al.* (2002) [36]. The genetic variants with the minor allele frequency of  $<0.01$  were removed from the analysis.